



SEQUENCE LISTING

COPY OF PAPERS
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<110> Wang, ^{Pavan}
Xi, Lei ^{TRADEMARK OFFICE}
Prosen, Dennis E.
MJ Bioworks, Inc.

<120> Improved Nucleic Acid Modifying Enzymes

<130> 020130-000111US

<140> US 09/870,353

<141> 2001-05-30

<150> US 60/207,567

<151> 2000-05-26

<150> US 09/640,958

<151> 2000-08-16

<160> 34

<170> PatentIn Ver. 2.1

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sequence non-specific double-stranded nucleic acid
binding protein Ssod7d

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<222> (1)..(189)

<223> Ssod7d

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sequence non-specific double-stranded nucleic acid
binding protein Ssod7d

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Ser Lys Ile Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr
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<223> Ssod7d-deltaTaq

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Gly Ala Val Ser Glu Lys Asp Ala Pro Lys Glu Leu Leu Gln Met Leu
50 55 60
Glu Lys Gln Lys Lys Gly Gly Val Thr Ser Pro Lys Ala Leu Glu
65 70 75 80
Glu Ala Pro Trp Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu
85 90 95
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100 105 110
Arg Gly Arg Val His Arg Ala Pro Glu Pro Tyr Lys Ala Leu Arg
115 120 125
Asp Leu Lys Glu Ala Arg Gly Leu Leu Ala Lys Asp Leu Ser Val Leu
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145 150 155 160
Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala
165 170 175
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180 185 190
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195 200 205
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225 230 235 240
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245 250 255
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260 265 270
Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Gly Leu Pro Ala Ile
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290 295 300
Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln Tyr
305 310 315 320
Arg Glu Leu Thr Lys Leu Lys Ser Thr Tyr Ile Asp Pro Leu Pro Asp
325 330 335
Leu Ile His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr
340 345 350
Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn
355 360 365
Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Ile
370 375 380
Ala Glu Glu Gly Trp Leu Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu
385 390 395 400
Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val
405 410 415
Phe Gln Glu Gly Arg Asp Ile His Thr Glu Thr Ala Ser Trp Met Phe
420 425 430
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Thr Ile Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser
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 500 505 510
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 Ssod7d/full-length Taq

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 Ssod7d/full-length Taq

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 35 40 45
 Gly Ala Val Ser Glu Lys Asp Ala Pro Lys Glu Leu Leu Gln Met Leu
 50 55 60
 Glu Lys Gln Lys Lys Gly Gly Val Thr Ser Gly Met Leu Pro Leu
 65 70 75 80
 Phe Glu Pro Lys Gly Arg Val Leu Leu Val Asp Gly His His Leu Ala
 85 90 95
 Tyr Arg Thr Phe His Ala Leu Lys Gly Leu Thr Thr Ser Arg Gly Glu
 100 105 110
 Pro Val Gln Ala Val Tyr Gly Phe Ala Lys Ser Leu Leu Lys Ala Leu
 115 120 125
 Lys Glu Asp Gly Asp Ala Val Ile Val Val Phe Asp Ala Lys Ala Pro
 130 135 140
 Ser Phe Arg His Glu Ala Tyr Gly Gly Tyr Lys Ala Gly Arg Ala Pro
 145 150 155 160
 Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala Leu Ile Lys Glu Leu Val
 165 170 175

Asp Leu Leu Gly Leu Ala Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp
 180 185 190
 Asp Val Leu Ala Ser Leu Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu
 195 200 205
 Val Arg Ile Leu Thr Ala Asp Lys Asp Leu Tyr Gln Leu Leu Ser Asp
 210 215 220
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 245 250 255
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 260 265 270
 Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu Glu Trp Gly Ser Leu Glu
 275 280 285
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 325 330 335
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 Glu Ala Pro Trp Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu
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 Gly Ala Arg Met Leu Leu Gln Val His Asp Glu Leu Val Leu Glu Ala
 850 855 860
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<220>
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 Pfu-Ssod7d

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 35 40 45
 Glu Glu Val Lys Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg
 50 55 60
 Ile Val Asp Val Glu Lys Val Glu Lys Phe Leu Gly Lys Pro Ile
 65 70 75 80
 Thr Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr Ile
 85 90 95
 Arg Glu Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr
 100 105 110
 Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
 115 120 125

Met Glu Gly Glu Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr
130 135 140
Leu Tyr His Glu Gly Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
145 150 155 160
Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn Ile
165 170 175
Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
180 185 190
Arg Phe Leu Arg Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Val Thr
195 200 205
Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu
210 215 220
Lys Leu Gly Ile Lys Leu Thr Ile Gly Arg Asp Gly Ser Glu Pro Lys
225 230 235 240
Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
245 250 255
His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro Thr
260 265 270
Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
275 280 285
Lys Val Tyr Ala Asp Glu Ile Ala Lys Ala Trp Glu Ser Gly Glu Asn
290 295 300
Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
305 310 315 320
Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg Leu
325 330 335
Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
340 345 350
Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala
355 360 365
Pro Asn Lys Pro Ser Glu Glu Tyr Gln Arg Arg Leu Arg Glu Ser
370 375 380
Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn
385 390 395 400
Ile Val Tyr Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Thr
405 410 415
His Asn Val Ser Pro Asp Thr Leu Asn Leu Glu Gly Cys Lys Asn Tyr
420 425 430
Asp Ile Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Ile Pro Gly
435 440 445
Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Lys Ile
450 455 460
Lys Thr Lys Met Lys Glu Thr Gln Asp Pro Ile Glu Lys Ile Leu Leu
465 470 475 480
Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Phe Tyr Gly
485 490 495
Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
500 505 510
Ser Val Thr Ala Trp Gly Arg Lys Tyr Ile Glu Leu Val Trp Lys Glu
515 520 525
Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
530 535 540
Leu Tyr Ala Thr Ile Pro Gly Gly Glu Ser Glu Glu Ile Lys Lys Lys
545 550 555 560
Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
565 570 575
Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
580 585 590
Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Val Ile Thr Arg Gly
595 600 605

Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
 610 615 620
 Ala Arg Val Leu Glu Thr Ile Leu Lys His Gly Asp Val Glu Glu Ala
 625 630 635 640
 Val Arg Ile Val Lys Glu Val Ile Gln Lys Leu Ala Asn Tyr Glu Ile
 645 650 655
 Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
 660 665 670
 Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala
 675 680 685
 Ala Lys Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
 690 695 700
 Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
 705 710 715 720
 Tyr Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
 725 730 735
 Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
 740 745 750
 Lys Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Thr Ser
 755 760 765
 Trp Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Ala Thr Val
 770 775 780
 Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile
 785 790 795 800
 Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu
 805 810 815
 Gly Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro
 820 825 830
 Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys
 835 840

<210> 9
 <211> 1904
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:fusion protein
 Sac7d-deltaTaq

<220>
 <221> CDS
 <222> (1)..(1904)
 <223> Sac7d-deltaTaq

<400> 9
 atgattacga attcgacggt gaaggtaaag ttcaagtata agggtaaaga gaaagaagta 60
 gacacttcaa agataaagaa ggtttgaga gtaggcaaaa tggtgtccct tacctatgac 120
 gacaatggta agacaggtag aggagctgta agcgagaaaag atgctccaaa agaattatta 180
 gacatgttag caagagcaga aagagagaag aaaggcggcg gtgtcaactag tcccaaggcc 240
 ctggaggagg ccccttggcc cccgcccggaa gggccttcg tgggcttgc gcttccccgc 300
 aaggagccca tgtggccga tcttctggcc ctggccggcc cgaggggggg ccgggtccac 360
 cgggcccccg agccttataa agccctcagg gacctgaagg aggccggggg gcttctcgcc 420
 aaagacctga gcgttctggc cctgaggggaa ggccttggcc tcccgcggg cgacgacccc 480
 atgctcctcg cttaccttcc ggacccttcc aacaccaccc ccgaggggggt ggcccgccgc 540
 tacggcgccc agtggacgggaa ggaggcgccc gagcggggccg ccctttccga gaggctttc 600
 gccaacctgt gggggaggct tgagggggag gagaggctcc tttggctta ccggggagggtg 660
 gagaggcccc tttccgctgt cctggcccac atggaggcca cgggggtgcg cctggacgtg 720
 gcctatctca gggccttgc cctggagggtg gccgaggaga tcgccccct cgaggccgg 780
 tcttccgcct ggccggccac cccttcaacc tcaactcccg ggaccagctg gaaagggtcc 840

tctttgacga gctaggcgctt cccgccatcg gcaagacgga gaagaccggc aagcgctcca 900
ccagcgcgcg cgtcctggag gccctccgcg agggccaccc catcgtaggag aagatcctgc 960
agtaccggga gtcaccaag ctgaagagca cttacattga ccccttgccg gacctcatcc 1020
accccaggac gggccgcctc cacacccgct tcaaccagac ggccacggcc acgggcaggc 1080
taagtagctc cgatccaaac ctccagaaca tccccgtccg caccggcgtt gggcagagga 1140
tccgcccggc cttcatcgcc gaggagggt ggctattggt ggccctggac tatagccaga 1200
tagagcttag ggtgctggcc cacctctccg ggcacgagaa cctgatccgg gtcttccagg 1260
aggggcggga catccacacg gagaccgcca gctggatgtt cggcgtcccc cgggaggccg 1320
tggacccctt gatgcgcgg gccgcacaaga ccatcaactt cggggtcctc tacggcatgt 1380
cggcccaccc cctctccag gagctagcca tcccttacga ggaggcccag gccttcattg 1440
agcgctactt tcagagctc cccaagggtgc gggcctggat tgagaagacc ctggaggagg 1500
gcaggaggcg ggggtacgtg gagaccctct tcggccgcg cgcgtacgtg ccagacctag 1560
aggcccgggt gaagagctg cgggaggcg ccgagcgcac ggccttcaac atgcccgtcc 1620
agggcaccgc cgccgacctc atgaagctgg ctatggtcaa gcttcccc aggctggagg 1680
aaatgggggc caggatgctc cttcaggtcc acgacgagct ggtcctcgag gccccaaaag 1740
agagggcgggaa ggccgtggcc cggctggcca aggaggtcat ggaggggggtg tatcccctgg 1800
ccgtccccctt ggaggtggag gtggggatag gggaggactg gctctccgccc aaggagggca 1860
ttgatggccg cggcggaggc gggcatcatc atcatcatca ttaa 1904

<210> 10
<211> 634
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:fusion protein
Sac7d-de_nTaq

<400> 10
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1 5 10 15
Glu Lys Glu Val Asp Thr Ser Lys Ile Lys Lys Val Trp Arg Val Gly
20 25 30
Lys Met Val Ser Phe Thr Tyr Asp Asp Asn Gly Lys Thr Gly Arg Gly
35 40 45
Ala Val Ser Glu Lys Asp Ala Pro Lys Glu Leu Leu Asp Met Leu Ala
50 55 60
Arg Ala Glu Arg Glu Lys Lys Gly Gly Val Thr Ser Pro Lys Ala
65 70 75 80
Leu Glu Glu Ala Pro Trp Pro Pro Glu Gly Ala Phe Val Gly Phe
85 90 95
Val Leu Ser Arg Lys Glu Pro Met Trp Ala Asp Leu Leu Ala Leu Ala
100 105 110
Ala Ala Arg Gly Gly Arg Val His Arg Ala Pro Glu Pro Tyr Lys Ala
115 120 125
Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu Ala Lys Asp Leu Ser
130 135 140
Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro Pro Gly Asp Asp Pro
145 150 155 160
Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly
165 170 175
Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Glu Ala Gly Glu Arg
180 185 190
Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu Trp Gly Arg Leu Glu
195 200 205
Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu Val Glu Arg Pro Leu
210 215 220
Ser Ala Val Leu Ala His Met Glu Ala Thr Gly Val Arg Leu Asp Val
225 230 235 240

Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala Glu Glu Ile Ala Arg
 245 250 255
 Leu Glu Ala Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn
 260 265 270
 Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Gly Leu Pro
 275 280 285
 Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala
 290 295 300
 Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu
 305 310 315 320
 Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr Tyr Ile Asp Pro Leu
 325 330 335
 Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn
 340 345 350
 Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Asp Pro Asn Leu
 355 360 365
 Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala
 370 375 380
 Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala Leu Asp Tyr Ser Gln
 385 390 395 400
 Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile
 405 410 415
 Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr Glu Thr Ala Ser Trp
 420 425 430
 Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro Leu Met Arg Arg Ala
 435 440 445
 Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg
 450 455 460
 Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Gln Ala Phe Ile
 465 470 475 480
 Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys
 485 490 495
 Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val Glu Thr Leu Phe Gly
 500 505 510
 Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg Val Lys Ser Val Arg
 515 520 525
 Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala
 530 535 540
 Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Glu
 545 550 555 560
 Glu Met Gly Ala Arg Met Leu Leu Gln Val His Asp Glu Leu Val Leu
 565 570 575
 Glu Ala Pro Lys Glu Arg Ala Glu Ala Val Ala Arg Leu Ala Lys Glu
 580 585 590
 Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val
 595 600 605
 Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu Gly Ile Asp Gly Arg
 610 615 620
 Gly Gly Gly His His His His His His
 625 630

<210> 11
 <211> 1965
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:fusion protein
 PL-deltaTaq

<220>
<221> CDS
<222> (1)..(1965)
<223> PL-deltaTaq

<400> 11

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gaggtagaca tctccaagat caagaaagta tggcggtgtgg gcaagatgat ctcccttcacc 180
tacgacgagg gcgggtggcaa gaccggccgt ggtgcggtaa gcgaaaaagga cgcgcgcaag 240
gagctgtcgc agatgctgga gaagcagaaaa aaggggcggcg gtgtcaccag tcccaaggcc 300
ctggaggagg cccctggcc cccgcccggaa ggggccttcg tgggctttgt gctttccgc 360
aaggagccca tggggccga tcttctggcc ctggccgccc ccaggggggg ccgggtccac 420
cgggcccccg agcctataa agccctcagg gacctaagg aggccgggg gcttctcgcc 480
aaagacctga gcgttctggc cctgaggaa ggcccttggcc tcccccggg cgacgacccc 540
atgctccctcg cctacctcct ggacccttcc aacaccaccc ccgagggggt ggcccggcgc 600
tacggccgggg agtggacgga ggaggccggg gagcgggccc cccttccga gaggctttc 660
gccaacctgt gggggaggct tgagggggag gagaggctcc ttggctta cccggaggtg 720
gagaggcccc ttccctgtc cctggcccac atggaggcca cgggggtgcg cttggacgtg 780
gcctatctca gggccttgtc cctggaggtg gccgaggaga tcgcccgcct cgaggccgag 840
gtcttccgcc tggccggcca ccccttcaac ctcaactccc gggaccagct ggaaagggtc 900
ctcttgcacg agcttagggct tccgcacatc gcaagacgg agaagacccg caagcgtcc 960
accagcgccg ccttcctgga ggcccctcgc gaggcccacc ccacgttggaa gaagatcctg 1020
cagtaccggg agtcaccaa gctgaagagc acctacattt accccttgcg ggacctcatc 1080
cacccccagga cggggccgcct ccacacccgc ttcaaccaga cggccacggc cacggcagg 1140
ctaagttagct ccgtatccaa cttccagaac atccctgtcc gcaccccgct tggcagagg 1200
atccgggggg cttcatcgc cgaggagggg tggttattgg tggcccttggaa ctatagccag 1260
atagagctca ggggtgtggc ccacccctcc ggcgacgaga acctgatccg ggttcccg 1320
gagggccggg acatccacac ggagaccgc agctggatgt tcggcgccccc cccggaggcc 1380
gtggaccccc tgatgcgccc ggccggcaag accatcaact tcggggtcct ctacggcatg 1440
tcggcccaacc gcctctccca ggagctagcc atcccttacg aggaggccca ggccttcatt 1500
gagcgctact ttcaagagctt ccccaaggtg cgggccttggaa ttgagaagac cttggaggag 1560
ggcaggaggg ggggtacgt ggagaccctc ttccggccgc gccgctacgt gccagaccta 1620
gaggccccggg tgaagagcgt gcgggaggcg gccgagcgca tggcccttcaa catggccgtc 1680
caggccaccc cggccgcacct catgaagctg gctatggtga agctttccc caggctggag 1740
gaaatggggg ccaggatgt cttcaggtc caccgacgac tggtcctcga ggccccaaaa 1800
gagagggcgg aggccgtggc cccgctggcc aaggaggtca tggaggggt gtatccccctg 1860
ggcgtgcggcc tggaggtgga ggtgggata ggggaggact ggcttcgcgc caaggagggc 1920
attgataacc gcaaggccgggg cggacatcat catcatcatc attaa 1965

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<210> 12
<211> 654
<212> PRT
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence:fusion protein
PL-deltaTag

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<400> 12
Met Ile Thr Asn Ser Lys Lys Lys Lys Lys Arg Lys Arg
      1          5          10          15
Lys Lys Lys Lys Gly Gly Val Thr Ser Gly Ala Thr Val Lys
      20          25          30
Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile Lys
      35          40          45
Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu Gly
      50          55          60
Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro Lys
      65          70          75          80

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Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys Gly Gly Gly Val Thr
 85 90 95
 Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala
 100 105 110
 Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala Asp Leu
 115 120 125
 Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala Pro Glu
 130 135 140
 Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu Ala
 145 150 155 160
 Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro Pro
 165 170 175
 Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr
 180 185 190
 Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Glu
 195 200 205
 Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu Trp
 210 215 220
 Gly Arg Leu Glu Gly Glu Arg Leu Leu Trp Leu Tyr Arg Glu Val
 225 230 235 240
 Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr Gly Val
 245 250 255
 Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala Glu
 260 265 270
 Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly His Pro
 275 280 285
 Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu
 290 295 300
 Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg Ser
 305 310 315 320
 Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val
 325 330 335
 Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr Tyr
 340 345 350
 Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu His
 355 360 365
 Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser
 370 375 380
 Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg
 385 390 395 400
 Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala Leu
 405 410 415
 Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp
 420 425 430
 Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr Glu
 435 440 445
 Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro Leu
 450 455 460
 Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly Met
 465 470 475 480
 Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala
 485 490 495
 Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala
 500 505 510
 Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val Glu
 515 520 525
 Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg Val
 530 535 540
 Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val
 545 550 555 560

Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe
565 570 575
Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val His Asp
580 585 590
Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val Ala Arg
595 600 605
Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro Leu
610 615 620
Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu Gly
625 630 635 640
Ile Asp Gly Arg Gly Gly His His His His His His His
645 650

<210> 13
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer L71F

<400> 13
cctgctctgc cgcttcacgc 20

<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer L71R

<400> 14
gcacagcgcc tggctgagga 20

<210> 15
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer L18015F

<400> 15
tgacggagga taacgccagc ag 22

<210> 16
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer L23474R

<400> 16
gaaagacgat gggtcgctaa tacgc 25

<210> 17
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer L18015F

<400> 17
tgacggagga taacgccagc ag

22

<210> 18
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer L29930R

<400> 18
ggggttggag gtcaatgggt tc

22

<210> 19
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer L30350F

<400> 19
cctgctctgc cgcttcacgc

20

<210> 20
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer L35121R

<400> 20
cacatggtag agcaaggctg gc

22

<210> 21
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer L2089F

<400> 21
cccgatatctg ctgggatact ggc

23

<210> 22
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer L7112R

<400> 22
cagcggtgct gactgaatca tgg

23

<210> 23
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer L30350F

<400> 23
cctgcctgcc gcacgc

19

<210> 24
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer L40547R

<400> 24
ccaatacccg tttcatcgcg gc

22

<210> 25
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer
H-Amelo-Y

<400> 25
ccacacctatc ctgggcacc

19

<210> 26
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial
Sequence:primer H-Amelo-YR

<400> 26
qcttgaggcc aaccatcaga gc

22

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<210> 27
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:human
      beta-globin primer Bglbn536F

<400> 27
ggttggccaa tctactccca gg

<210> 28
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:human
      beta-globin primer Bglbn536R

<400> 28
gctcaactcag tgtggcaaag

<210> 29
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:human
      beta-globin primer Bglbn1408R

<400> 29
gattagcaaa agggcctagc ttgg

<210> 30
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:6-His epitope
      tag

<400> 30
His His His His His His
    1           5

<210> 31
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:anti-DYKDDDDK
      epitope tag
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22

20

24

<400> 31
Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 32
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:peptide linker

<400> 32
Gly Gly Val Thr
1

<210> 33
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:peptide linker

<400> 33
Gly Thr Gly Gly Gly Gly
1 5

<210> 34
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:lysine-rich peptide

<400> 34
Asn Ser Lys Lys Lys Lys Lys Lys Arg Lys Lys Arg Lys Lys Lys
1 5 10 15
Gly Gly Gly Val Thr
20